

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/076,157A
Source: IFW/6
Date Processed by STIC: 10/22/04

ENTERED



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/076,157A

DATE: 10/22/2004

TIME: 12:20:07

Input Set : A:\076157.txt

Output Set: N:\CRF4\10222004\J076157A.raw

```

3 <110> APPLICANT: Pompejus, Markus
4 Seulberger, Harald
5 Hoeffken, Hans Wolfgang
6 Doval, Jose Luis Revuelta
7 Jimenez, Alberto
8 Garcia, Maria Angeles Santos
10 <120> TITLE OF INVENTION: Phosphoriboxyl-Pyrophosphate Synthetase Polypeptide
12 <130> FILE REFERENCE: PF48687-2/DP
14 <140> CURRENT APPLICATION NUMBER: US 10/076,157A
15 <141> CURRENT FILING DATE: 2002-02-15
17 <150> PRIOR APPLICATION NUMBER: Germany, 19757755.5
18 <151> PRIOR FILING DATE: 1997-12-23
20 <160> NUMBER OF SEQ ID NOS: 21
22 <170> SOFTWARE: WordPerfect 8
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1911
26 <212> TYPE: DNA
27 <213> ORGANISM: Ashbya gossypii
29 <400> SEQUENCE: 1
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32 gcatccgtat cgcggggcggg tggaaatgggt aatcattagg aaacaccaat gtcccatgggt 120
33 attgtccgtc ctcgtatgggt gtctcaggag gaccgggtat cacgtatgtc cacaccagga 180
34 tattgtcttc ctttgggtgtt gccacatgtt agggcggggg gtttcgttcc atcattttgt 240
35 actcccttga gagccgcttg tacgactgtc ttgtatgcat tttccatcttactt attagttct 300
36 caccacttcc cgccaaacaa tctgcacttt acgagcgctt tctatccctc gggtcgtct 360
37 agttgattat tggcgaaact gatagttcag gtacttccat gatgcgggtca tatccacgt 420
38 tgtgatcag tgatcatcag ccatgtgtcc agtcacggg cctgcctaca ctattggagg 480
39 ctctgtgagt catgatttat tgcataatcaa gcccagatag tcgttggggta tactaccgtt 540
40 gcccgatgatgatcgtttaatggatgatcgtttaatggatgatcgtttaatggatgatcgtttaaca 600
41 gttatttgacg ccgcaatccat acgccatgatcgtttaatggatgatcgtttaatggatgatcgtttaaca 652
42 Met Ser Ser Asn Ser Ile Lys Leu Leu
43 1 5
44 gca ggt aac tcg cac ccg gac cta gct gag aag gtc tcc gtt cgc cta 700
45 Ala Gly Asn Ser His Pro Asp Leu Ala Glu Lys Val Ser Val Arg Leu
46 10 15 20 25
47 ggt gta cca ctt tcg aag att gga gtg tat cac tac tct aac aaa gag 748
48 Gly Val Pro Leu Ser Lys Ile Gly Val Tyr His Tyr Ser Asn Lys Glu
49 30 35 40
50 acg tca gtt act atc ggc gaa agt atc cgt gat gaa gat gtc tac atc 796
51 Thr Ser Val Thr Ile Gly Glu Ser Ile Arg Asp Glu Asp Val Tyr Ile
52 45 50 55
53 atc cag aca gga acg ggg gag cag gaa atc aac gac ttc ctc atg gaa 844
54 Ile Gln Thr Gly Thr Gly Glu Gln Glu Ile Asn Asp Phe Leu Met Glu

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69	60	65	70	
71	ctg ctc atc atc cat gcc tgc cgg tca gcc tct gcg cgg aag atc			892
72	Leu Leu Ile Met Ile His Ala Cys Arg Ser Ala Ser Ala Arg Lys Ile			
73	75	80	85	
75	aca gcg gtt ata cca aac ttc cct tac gca aga caa gac aaa aag gac			940
76	Thr Ala Val Ile Pro Asn Phe Pro Tyr Ala Arg Gln Asp Lys Lys Asp			
77	90	95	100	105
79	aag tcg cga gca ccg ata act gcc aag ctg gtg gcc aag atg cta gag			988
80	Lys Ser Arg Ala Pro Ile Thr Ala Lys Leu Val Ala Lys Met Leu Glu			
81	110	115	120	
83	acc gcg ggg tgc aac cac gtt atc acg atg gat ttg cac gcg tct caa			1036
84	Thr Ala Gly Cys Asn His Val Ile Thr Met Asp Leu His Ala Ser Gln			
85	125	130	135	
87	att cag ggt ttc ttc cac att cca gtg gac aac cta tat gca gag ccg			1084
88	Ile Gln Gly Phe Phe His Ile Pro Val Asp Asn Leu Tyr Ala Glu Pro			
89	140	145	150	
91	aac atc ctg cac tac atc caa cat aat gtg gac ttc cag aat agt atg			1132
92	Asn Ile Leu His Tyr Ile Gln His Asn Val Asp Phe Gln Asn Ser Met			
93	155	160	165	
95	ttg gtc gcg cca gac gcg ggg tgc gcg aag cgc acg tgc acg ctt tcg			1180
96	Leu Val Ala Pro Asp Ala Gly Ser Ala Lys Arg Thr Ser Thr Leu Ser			
97	170	175	180	185
99	gac aag ctg aat ctc aac ttc gcg ttg atc cac aaa gaa ccg cag aag			1228
100	Asp Lys Leu Asn Leu Asn Phe Ala Leu Ile His Lys Glu Arg Gln Lys			
101	190	195	200	
103	gcg aac gag gtc tgc cgg atg gtg ttg gtg ggt gat gtc gcc gac aag			1276
104	Ala Asn Glu Val Ser Arg Met Val Leu Val Gly Asp Val Ala Asp Lys			
105	205	210	215	
107	tcc tgt att att gta gac gac atg gcg gac acg tgc gga acg cta gtg			1324
108	Ser Cys Ile Ile Val Asp Asp Met Ala Asp Thr Cys Gly Thr Leu Val			
109	220	225	230	
111	aag gcc act gac acg ctg atc gaa aat tgt gcg aaa gaa gtg att gcc			1372
112	Lys Ala Thr Asp Thr Leu Ile Glu Asn Cys Ala Lys Glu Val Ile Ala			
113	235	240	245	
115	att gtg aca cac ggt ata ttt tct ggc ggc gcc cgc gag aag ttg cgc			1420
116	Ile Val Thr His Gly Ile Phe Ser Gly Gly Ala Arg Glu Lys Leu Arg			
117	250	255	260	265
119	aac agc aag ctg gca cgg atc gta agc aca aat acg gtg cca gtg gac			1468
120	Asn Ser Lys Leu Ala Arg Ile Val Ser Thr Asn Thr Val Pro Val Asp			
121	270	275	280	
123	ctc aat cta gat atc tac cac caa att gac att agt gcc att ttg gcc			1516
124	Leu Asn Leu Asp Ile Tyr His Gln Ile Asp Ile Ser Ala Ile Leu Ala			
125	285	290	295	
127	gag gca att aga agg ctt cac aac ggg gaa agt gtg tgc tac ctg ttc			1564
128	Glu Ala Ile Arg Arg Leu His Asn Gly Glu Ser Val Ser Tyr Leu Phe			
129	300	305	310	
131	aat aac gct gtc atg tagtgctgtc agtggcagat gcatgatcgc tggcctaatt			1619
132	Asn Asn Ala Val Met			
133	315			

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135 atctgtgtaa gttgatacaa tgcagtaaat acagtacata aaactgaatg ttttcactt 1679
 137 aggggtgcctt tggttgcctg atagcgtgtg tgcaatttg gaggtgaaag ttgaacatca 1739
 139 cgtaatgaat acaaacaaga ttgcacatta ggaaaagcga taaatttattt attatttgc 1799
 141 actggcctt gagcgtttaa gcctgaacat tttgccctt ttgtttgacc gtaccgttat 1859
 143 cactcgtcct tatatatggc tatccttctc ttccggaact tcttcgagcg ta 1911
 146 <210> SEQ ID NO: 2
 147 <211> LENGTH: 318
 148 <212> TYPE: PRT
 149 <213> ORGANISM: Ashbya gossypii
 151 <400> SEQUENCE: 2
 153 Met Ser Ser Asn Ser Ile Lys Leu Leu Ala Gly Asn Ser His Pro Asp
 154 1 5 10 15
 156 Leu Ala Glu Lys Val Ser Val Arg Leu Gly Val Pro Leu Ser Lys Ile
 157 20 25 30
 159 Gly Val Tyr His Tyr Ser Asn Lys Glu Thr Ser Val Thr Ile Gly Glu
 160 35 40 45
 162 Ser Ile Arg Asp Glu Asp Val Tyr Ile Ile Gln Thr Gly Thr Gly Glu
 163 50 55 60
 165 Gln Glu Ile Asn Asp Phe Leu Met Glu Leu Leu Ile Met Ile His Ala
 166 65 70 75 80
 168 Cys Arg Ser Ala Ser Ala Arg Lys Ile Thr Ala Val Ile Pro Asn Phe
 169 85 90 95
 171 Pro Tyr Ala Arg Gln Asp Lys Lys Asp Lys Ser Arg Ala Pro Ile Thr
 172 100 105 110
 174 Ala Lys Leu Val Ala Lys Met Leu Glu Thr Ala Gly Cys Asn His Val
 175 115 120 125
 177 Ile Thr Met Asp Leu His Ala Ser Gln Ile Gln Gly Phe Phe His Ile
 178 130 135 140
 180 Pro Val Asp Asn Leu Tyr Ala Glu Pro Asn Ile Leu His Tyr Ile Gln
 181 145 150 155 160
 183 His Asn Val Asp Phe Gln Asn Ser Met Leu Val Ala Pro Asp Ala Gly
 184 165 170 175
 186 Ser Ala Lys Arg Thr Ser Thr Leu Ser Asp Lys Leu Asn Leu Asn Phe
 187 180 185 190
 189 Ala Leu Ile His Lys Glu Arg Gln Lys Ala Asn Glu Val Ser Arg Met
 190 195 200 205
 192 Val Leu Val Gly Asp Val Ala Asp Lys Ser Cys Ile Ile Val Asp Asp
 193 210 215 220
 195 Met Ala Asp Thr Cys Gly Thr Leu Val Lys Ala Thr Asp Thr Leu Ile
 196 225 230 235 240
 198 Glu Asn Cys Ala Lys Glu Val Ile Ala Ile Val Thr His Gly Ile Phe
 199 245 250 255
 201 Ser Gly Gly Ala Arg Glu Lys Leu Arg Asn Ser Lys Leu Ala Arg Ile
 202 260 265 270
 204 Val Ser Thr Asn Thr Val Pro Val Asp Leu Asn Leu Asp Ile Tyr His
 205 275 280 285
 207 Gln Ile Asp Ile Ser Ala Ile Leu Ala Glu Ala Ile Arg Arg Leu His
 208 290 295 300
 210 Asn Gly Glu Ser Val Ser Tyr Leu Phe Asn Asn Ala Val Met

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Input Set : A:\076157.txt
Output Set: N:\CRF4\10222004\J076157A.raw

211	305	310	315														
214	<210> SEQ ID NO: 3																
215	<211> LENGTH: 5369																
216	<212> TYPE: DNA																
217	<213> ORGANISM: Ashbya gossypii																
219	<400> SEQUENCE: 3																
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223								Met									
224								1									
226	gat	cgt	ggt	tgt	aaa	ggt	atc	tct	tat	gtg	ctc	agt	gca	atg	gtt	ttt	105
227	Asp	Arg	Gly	Cys	Lys	Gly	Ile	Ser	Tyr	Val	Leu	Ser	Ala	Met	Val	Phe	
228							5			10			15				
230	cac	ata	ata	ccg	att	aca	ttt	gaa	ata	tcg	atg	gta	tgt	ggc	ata	ttg	153
231	His	Ile	Ile	Pro	Ile	Thr	Phe	Glu	Ile	Ser	Met	Val	Cys	Gly	Ile	Leu	
232							20			25			30				
234	aca	taa	cag	ttt	ggt	gct	tcc	ttc	gct	ata	aca	ttc	tcg	act	atg	201	
235	Thr	Tyr	Gln	Phe	Gly	Ala	Ser	Phe	Ala	Ala	Ile	Thr	Phe	Ser	Thr	Met	
236							35			40			45				
238	ctt	ctt	ttc	atc	ttt	act	ttc	aga	acg	acg	gct	ttt	tcg	ttt	ccg	aca	249
239	Leu	Leu	Tyr	Ser	Ile	Phe	Thr	Phe	Arg	Thr	Thr	Ala	Trp	Arg	Thr	Arg	
240							50			55			60			65	
242	ttt	agg	cgt	gat	gct	aac	aag	gct	gac	aat	aag	gcc	gct	agt	gtg	gca	297
243	Phe	Arg	Arg	Asp	Ala	Asn	Lys	Ala	Asp	Asn	Lys	Ala	Ala	Ser	Val	Ala	
244							70			75			80				
246	ttg	gat	tcc	cta	ata	aat	ttt	gaa	gct	gta	aag	tat	ttc	aat	aac	gag	345
247	Leu	Asp	Ser	Leu	Ile	Asn	Phe	Glu	Ala	Val	Lys	Tyr	Phe	Asn	Asn	Glu	
248							85			90			95				
250	aag	taa	ctt	gct	gac	aag	tat	cac	aca	tcc	ttt	atg	aag	taa	ccg	gat	393
251	Lys	Tyr	Leu	Ala	Asp	Lys	Tyr	His	Thr	Ser	Leu	Met	Lys	Tyr	Arg	Asp	
252							100			105			110				
254	tcc	cag	ata	aag	gtc	tcg	caa	tcg	ctg	gct	ttt	ttt	ttt	ttt	ttt	ttt	441
255	Ser	Gln	Ile	Lys	Val	Ser	Gln	Ser	Leu	Ala	Phe	Leu	Asn	Thr	Gly	Gln	
256							115			120			125				
258	aac	cta	att	ttt	acc	act	gca	ctg	act	gca	atg	atg	tat	atg	gcc	tgt	489
259	Asn	Leu	Ile	Phe	Thr	Thr	Ala	Leu	Thr	Ala	Met	Met	Tyr	Met	Ala	Cys	
260							130			135			140			145	
262	aat	ggt	gtt	atg	cag	ggc	tct	aca	gtt	ggg	gat	ctt	gtg	tta	att	537	
263	Asn	Gly	Val	Met	Gln	Gly	Ser	Leu	Thr	Val	Gly	Asp	Leu	Val	Leu	Ile	
264							150			155			160				
266	aat	caa	ctg	gta	ttc	cag	ctc	tcc	gtt	cca	cta	aac	ttc	ttt	ggt	agc	585
267	Asn	Gln	Leu	Val	Phe	Gln	Leu	Ser	Val	Pro	Leu	Asn	Phe	Leu	Gly	Ser	
268							165			170			175				
270	gtc	tac	cgt	gat	ctc	aag	cag	tct	ctg	ata	gat	atg	gaa	tct	tta	ttt	633
271	Val	Tyr	Arg	Asp	Leu	Lys	Gln	Ser	Leu	Ile	Asp	Met	Glu	Ser	Leu	Phe	
272							180			185			190				
274	aaa	ctg	caa	aaa	aat	cag	gtc	aca	att	aag	aac	tcc	cca	aat	gcc	cag	681
275	Lys	Leu	Gln	Lys	Asn	Gln	Val	Thr	Ile	Lys	Asn	Ser	Pro	Asn	Ala	Gln	
276							195			200			205				
278	aac	cta	cca	ata	cac	aaa	ccg	ttt	gat	att	cgc	ttt	gaa	aat	gtt	acg	729

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279	Asn	Leu	Pro	Ile	His	Lys	Pro	Leu	Asp	Ile	Arg	Phe	Glu	Asn	Val	Thr	
280	210						215				220				225		
282	ttt	ggc	tat	gac	ccg	gag	cg	cg	ata	ttg	aac	aat	gtt	tcg	ttt	acc	777
283	Phe	Gly	Tyr	Asp	Pro	Glu	Arg	Arg	Ile	Leu	Asn	Asn	Val	Ser	Phe	Thr	
284							230				235				240		
286	atc	cca	gct	gga	atg	aag	act	gcc	ata	gta	ggc	cca	tcg	ggc	tcg	ggg	825
287	Ile	Pro	Ala	Gly	Met	Lys	Thr	Ala	Ile	Val	Gly	Pro	Ser	Gly	Ser	Gly	
288							245				250				255		
290	aag	tcc	acc	att	ttg	aag	ctc	gta	ttt	aga	ttc	tat	gag	ccc	gag	caa	873
291	Lys	Ser	Thr	Ile	Leu	Lys	Leu	Val	Phe	Arg	Phe	Tyr	Glu	Pro	Glu	Gln	
292							260				265				270		
294	ggt	cgt	atc	cta	gtt	ggc	ggc	aca	gat	atc	cgc	gat	tta	gac	ttg	ctt	921
295	Gly	Arg	Ile	Leu	Val	Gly	Gly	Thr	Asp	Ile	Arg	Asp	Leu	Asp	Leu	Leu	
296							275				280				285		
298	tct	tta	cg	aag	gct	atc	gg	gtc	gt	ccc	caa	gat	act	cct	ctc	tcc	969
299	Ser	Leu	Arg	Lys	Ala	Ile	Gly	Val	Val	Pro	Gln	Asp	Thr	Pro	Leu	Phe	
300							290				295				300		
302	aat	gac	aca	atc	tgg	gag	aat	gtt	aaa	ttc	ggc	aat	atc	agt	tcc	tct	1017
303	Asn	Asp	Thr	Ile	Trp	Glu	Asn	Val	Lys	Phe	Gly	Asn	Ile	Ser	Ser	Ser	
304							310				315				320		
306	gac	gat	gag	att	ctc	agg	gcc	ata	gaa	aaa	gct	caa	ctc	acg	aag	cta	1065
307	Asp	Asp	Glu	Ile	Leu	Arg	Ala	Ile	Glu	Lys	Ala	Gln	Leu	Thr	Lys	Leu	
308							325				330				335		
310	ctc	cag	aac	cta	cca	aag	ggc	gct	tcc	acc	gtt	gta	ggg	gag	cgc	gg	1113
311	Leu	Gln	Asn	Leu	Pro	Lys	Gly	Ala	Ser	Thr	Val	Val	Gly	Glu	Arg	Gly	
312							340				345				350		
314	ttg	atg	atc	agc	gga	gg	gag	aaa	caa	agg	ctt	gct	att	gct	cgt	gt	1161
315	Leu	Met	Ile	Ser	Gly	Gly	Glu	Lys	Gln	Arg	Leu	Ala	Ile	Ala	Arg	Val	
316							355				360				365		
318	ctt	ttg	aag	gac	gct	ccg	ctg	atg	ttt	ttc	gac	gag	gct	aca	agt	gct	1209
319	Leu	Leu	Lys	Asp	Ala	Pro	Leu	Met	Phe	Phe	Asp	Glu	Ala	Thr	Ser	Ala	
320							370				375				385		
322	ctg	gat	aca	cac	aca	gag	cag	gca	ctc	ttg	cac	acc	att	cag	cag	aac	1257
323	Leu	Asp	Thr	His	Thr	Glu	Gln	Ala	Leu	Leu	His	Thr	Ile	Gln	Gln	Asn	
324							390				395				400		
326	ttt	tct	tcc	aat	tca	aag	acg	acg	gtt	tac	gtt	gcc	cat	aga	ctg	cgc	1305
327	Phe	Ser	Ser	Asn	Ser	Lys	Thr	Ser	Val	Tyr	Val	Ala	His	Arg	Leu	Arg	
328							405				410				415		
330	aca	atc	gct	gat	gca	gat	aag	atc	att	gtt	ctt	gaa	caa	gg	tct	gtc	1353
331	Thr	Ile	Ala	Asp	Ala	Asp	Lys	Ile	Ile	Val	Leu	Glu	Gln	Gly	Ser	Val	
332							420				425				430		
334	cgc	gaa	gag	ggc	aca	cac	agc	tcg	ctg	tta	gca	caa	gga	tcc	cta		1401
335	Arg	Glu	Glu	Gly	Thr	His	Ser	Ser	Leu	Leu	Ala	Ser	Gln	Gly	Ser	Leu	
336							435				440				445		
338	tac	cg	gg	gt	ctg	tgg	gat	att	cag	gaa	aac	cta	acg	ctt	ccg	gg	1449
339	Tyr	Arg	Gly	Leu	Trp	Asp	Ile	Ile	Val	Leu	Glu	Asn	Leu	Thr	Leu	Pro	Arg
340							450				455				460		
342	cct	gag	cag	tca	acc	gga	tct	cag	cat	gca	tagacgtctg	actagagatt					1499
343	Pro	Glu	Gln	Ser	Thr	Gly	Ser	Gln	Gln	His	Ala						

VERIFICATION SUMMARY
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Input Set : A:\076157.txt
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L:31 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=1
L:222 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=3
L:356 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:496 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:500 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:504 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:508 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:512 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:516 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:520 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:524 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:528 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:532 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:536 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:540 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:544 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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L:552 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:556 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:560 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:564 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:568 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:572 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:576 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:580 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:584 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:588 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:902 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=7
L:976 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:1229 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=10
L:1515 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=12